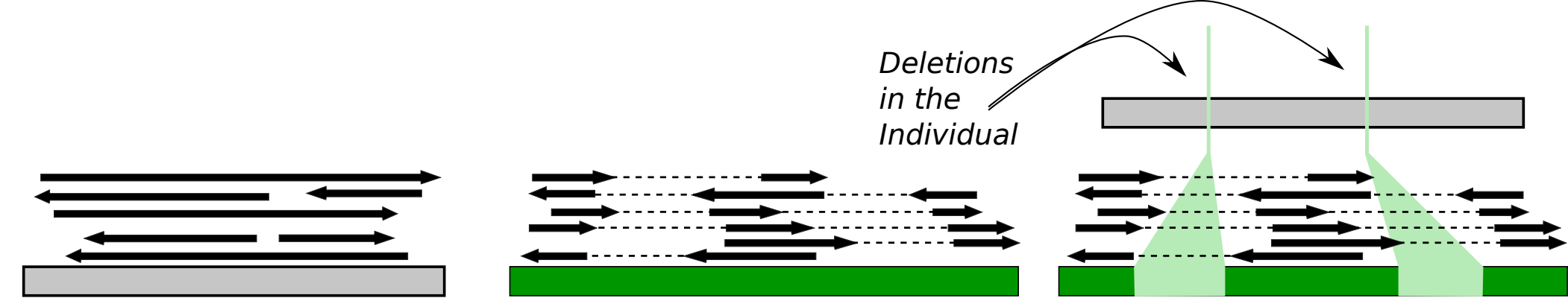

1. Sequence reads from individual genome using any sequencing platform

2. Align reads to reference genome; reads may map to different locations

3. Determine SVs from the alignments and compute novel adjacency probabilities